

Exhibit B

Marked Up Version of Amended Claims in U.S. Patent Application Ser. No. 09/783,669

1. (Amended) An isolated nucleic acid molecule comprising a nucleotide sequence that:
 - (a) encodes the amino acid sequence shown in SEQ ID NO: 4; and
 - (b) hybridizes under highly stringent conditions to the complement of the nucleotide sequence of SEQ ID NO: 3 [or the complement thereof].
- 2.(Amended) An [isolated nucleic acid] expression vector [having the property of being capable of expressing] comprising a nucleic acid sequence encoding the amino acid sequence shown in SEQ ID NO:4.
- 3.(Amended) An [isolated nucleic acid] expression vector [having the property of being capable of expressing] comprising a nucleic acid sequence encoding the amino acid sequence shown in SEQ ID NO:2.
- 4.(Amended) An [isolated nucleic acid] expression vector [having the property of being capable of expressing] comprising a nucleic acid sequence encoding the amino acid sequence shown in SEQ ID NO:6.
- 5.(New) A cell comprising the expression vector of Claim 2.
- 6.(New) A cell comprising the expression vector of Claim 3.
- 7.(New) A cell comprising the expression vector of Claim 4.

Exhibit B
Seq Id No:1 versus human genome

Home

Paracel BLAST Results

Help

MEGABLAST 1.2.3-Paracel [2001-11-20]

Reference:

Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000),
"A greedy algorithm for aligning DNA sequences",
J Comput Biol 2000; 7(1-2):203-14.

Database: Homo_sapiens.latestgp.masked.fa
33,840 sequences; 200,810,911,373 total letters

Query= hGPR_32 = Seq Id No:1
(813 letters)

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Sequences producing significant alignments:

Score (bits)	E Value
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AC027026.10.1.155376	1138	0.0
AC023078.9.1.163718	238	4e-60
AC107948.7.1.156839	216	2e-53
AC090099.14.1.172939	216	2e-53
AC103974.6.1.189230	212	3e-52

>AC027026.10.1.155376
Length = 155376

Score = 1138 bits (574), Expect = 0.0
Identities = 574/574 (100%)
Strand = Plus / Minus

Query: 1 atggatccaaccaccccggcctggggaacagaaagtacaacagtgaatggaaatgaccaa 60
|||||
Sbjct: 31187 atggatccaaccaccccggcctggggaacagaaagtacaacagtgaatggaaatgaccaa 31128

Query: 61 gcccttcttctgctttgtggcaaggagaccctgatcccggtcttctgatccttttcatt 120
|||||
Sbjct: 31127 gcccttcttctgctttgtggcaaggagaccctgatcccggtcttctgatccttttcatt 31068

Query: 121 gccctggtcgggctggtaggaaacgggtttgtgctctggctcctgggcttccgcatgcgc 180
|||||
Sbjct: 31067 gccctggtcgggctggtaggaaacgggtttgtgctctggctcctgggcttccgcatgcgc 31008

Query: 181 aggaacgccttctctgtctacgtcctcagcctggccggggccgacttctcttctctgc 240
|||||
Sbjct: 31007 aggaacgccttctctgtctacgtcctcagcctggccggggccgacttctcttctctgc 30948

Query: 241 ttccagattataaattgcctggtgtacctcagtaacttcttctgttccatctccatcaat 300
|||||
Sbjct: 30947 ttccagattataaattgcctggtgtacctcagtaacttcttctgttccatctccatcaat 30888

Query: 301 ttccctagcttcttccaccactgtgatgacctgtgcctaccttgaggcctgagcatgctg 360
|||||

Sbjct: 30887 ttccctagctttcttcaccactgtgatgacctgtgcctaccttgaggcctgagcatgctg 30828

Query: 361 agcacgcgtcagcacccgagcgctgcctgtccgtcctgtggcccatctggtatcgctgccgc 420
|||||

Sbjct: 30827 agcacgcgtcagcacccgagcgctgcctgtccgtcctgtggcccatctggtatcgctgccgc 30768

Query: 421 cgccccagacacctgtcagcggtcggtgtgtgtcctgctctgggccctgtccctactgctg 480
|||||

Sbjct: 30767 cgccccagacacctgtcagcggtcggtgtgtgtcctgctctgggccctgtccctactgctg 30708

Query: 481 agcatcttggaagggaagttctgtggcttcttatttagtgatgggtgactctgggtgggtgt 540
|||||

Sbjct: 30707 agcatcttggaagggaagttctgtggcttcttatttagtgatgggtgactctgggtgggtgt 30648

Query: 541 cagacatttgatttcatcactgcagcggtggctga 574
|||||

Sbjct: 30647 cagacatttgatttcatcactgcagcggtggctga 30614

Score = 442 bits (223), Expect = e-121
Identities = 230/232 (99%), Gaps = 1/232 (0%)
Strand = Plus / Minus

Query: 582 attcatggttctctgtgggtccagtcctggccctgctgggtcaggatcctctgtgggtccag 641
|||||

Sbjct: 30606 attcatggttctctgtgggtccagtcctggccctgctgggtcaggatcctctgtgggtccag 30547

Query: 642 gggctctgccactgaccaggctgtacctgaccatcctgctcacagtgcctgggtgttcctcct 701
|||||

Sbjct: 30546 gggctctgccactgaccaggctgtacctgaccatcctgctcacagtgcctgggtgttcctcct 30487

Query: 702 ctgcggcctgcccttttggcattcagtggttcctaataattatggatctggaaggattctga 761
|||||

Sbjct: 30486 ctgcggcctgcccttttggcattcagtggttcctaataattatggatctggaaggattctga 30427

Query: 762 tgtcttatttttggcatattcatccaagtttcagttgtcctgtcatctcttaa 813
|||||

Sbjct: 30426 tgtcttatttttgtcatattcatcc-agtttcagttgtcctgtcatctcttaa 30376

>AC023078.9.1.163718
Length = 163718

Score = 238 bits (120), Expect = 4e-60
Identities = 212/242 (87%), Gaps = 4/242 (1%)
Strand = Plus / Minus

Query: 335 cctaccttgaggcctgagcatgctgagcacgcgtcagcacccgagcgctgcctgtccgtcc 394
|||||

Sbjct: 71224 cctactttgcaggcctgagctttctgagtgccgtgagcaccgagcgctgcctgtccgtcc 71165

Query: 395 tgtggcccatctggtatcgctgccgcccagacacctgtcagcggtcgtgtgtgtcc 454
|||||

Sbjct: 71164 tgtggcccatctggtaccgctgccaccgcccacacacctgtcagcggtggtgtgtgtcc 71105

Query: 455 tgctctggggccctgtccctactgctgagcatcttgaag-ggaagttctgtggcttctta 513
|||||

Sbjct: 71104 tgctctggggccctgtccctgctgaggagcatcctgga-gtggatgttatgtggcttctg 71046

Query: 514 tttagtgatggtgactctggttgggtgcagacatttgatttcatcactg-cagcggtggct 572
|| |||

Sbjct: 71045 ttcagtgggtgctgattctgcttgggtgtcaaacatcagatttcatcacagtc-gcgtggct 70987

Query: 573 ga 574
||

Sbjct: 70986 ga 70985

Score = 222 bits (112), Expect = 3e-55
Identities = 206/236 (87%), Gaps = 7/236 (2%)
Strand = Plus / Minus

Query: 344 caggcctgagcatgctgagcaccgtcagcaccgagcgctgcctgtccgtcctgtggcca 403
|||||

Sbjct: 24330 caggcctgagcatgctgagcaccatcagcaccgagcaccgctgcctgtccgtcctgtggcca 24271

Query: 404 tctggtatc-gctgccgcccagacacctgtcagcggtcgtgtgtgtcctgctctgg 462
|||||

Sbjct: 24270 tctggta-ctgctgccactgcccacacacctgtcagcggtcatgtgtgtcctgctctgg 24212

Query: 463 gccctgtccctactgctgagcatcttgaag-ggaagttctgtggcttcttatttagtga 521
|||||

Sbjct: 24211 gccctgtccctgttgcagagcatcctgga-gtggatgttctgtagcttctgttttagtga 24153

Query: 522 tgggtgactctggt--t-ggtgtcagacatttgatttcatcactgcagcggtggctga 574
|| |||

Sbjct: 24152 tgttgactctgataattgggtgtcaaataattagatttcctcactgctgtgtggctga 24097

Score = 212 bits (107), Expect = 3e-52
Identities = 214/249 (85%), Gaps = 4/249 (1%)
Strand = Plus / Minus

Query: 313 ttcaccactgtgatgacctgtgc-ctaccttgcaggcctgagcatgctgagcaccgtcag 371
|||||

Sbjct: 963 ttcaccactgtgatgacct-ttctctactttacaggcctgagcatgctgggctccatcag 905

Query: 372 caccgagcgctgcctgtccgtcctgtggcccatctggtatcgctgccgcccagaca 431
||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 904 caccaagcactgcctgtccatcctgtggcccatctagtaccgctgccaccacccacaca 845

Query: 432 cctgtcagcggcgtgtgtgtgtcctgtctgtggccctgtccctactgctgagcatcttga 491
||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 844 cctgtcagcagtc--gtgtgtcctgtctgtggccctgtccctgctgcagagcatcctga 787

Query: 492 aggggaagttctgtggcttcttatttagtgatggtgactctggttggtgtcagacatttga 551
| ||| ||||| ||||| ||| ||||| || ||| ||||| ||||| ||||| ||||| |||||
Sbjct: 786 atggatgttctgtggcttctgtctagtgtggtgctgattctgtttggtgtgaaacatcaga 727

Query: 552 tttcatcac 560
|||||
Sbjct: 726 tttcatcac 718

Score = 190 bits (96), Expect = 9e-46
Identities = 208/244 (85%), Gaps = 7/244 (2%)
Strand = Plus / Minus

Query: 320 ctgtgatgacctgtgcctacctt-gcaggcctgagcatgctgagcaccgtcagcaccgag 378
||||| ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 47852 ctgtgatgacctttcccta-cttggcaggcctgaatattctgagtgccatgagcaccaag 47794

Query: 379 cgctgcctgtccgtcctgtggcccatctggtatcgctgccgcccagacacctgtca 438
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 47793 cgctgcctgtcaatcctgtggcccatctggtaacgctgccgccacccacacacctgtca 47734

Query: 439 gcggtcgtgtgtgtcctgtctgtggccctgtccctactgct-gagcatcttgaag-gga 496
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 47733 acggtcgtgtgtgtcctgtctgtggccctgtccctgctg-tagagcatcctgga-gtgga 47676

Query: 497 agttctgtggcttcttatttagtgatggtgactctggttggtgtcagacatttgatttca 556
||||| ||| ||| ||||| ||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 47675 tgttctgtgactccctgttttagtgatgctgattctgtttggtgtcaaacatcagatt-ca 47617

Query: 557 tcac 560
|||
Sbjct: 47616 tcac 47613

Score = 186 bits (94), Expect = 1e-44
Identities = 190/221 (85%), Gaps = 6/221 (2%)
Strand = Plus / Minus

Query: 344 caggcctgagcatgctgagcaccgtcagcaccgagcgctgcctgtccgtcctgtggcca 403
||||| ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 109133 caggcctgagcttctgagtccatgagcaccgagcgctgcctgtgcgtcctgtggcca 109074

Query: 404 tctggtatcgctgccgcccgc--agacacctgtcagcggtcgtgtgtgtcctgctctg 461
|||||
Sbjct: 109073 tctggtaccgctgcctcctccccccacacacctgtcagcggtcgtgtgtgtcctgctttg 109014

Query: 462 ggccctgtccctactgctgagcatcttgaaggga-gttctgtggcttcttatttagtg 520
|||||
Sbjct: 109013 ggccctgtccctactgcggagcatcctgga-gtgaatgttctgtgacttctgttttagtg 108955

Query: 521 atggtgactctggttggtgtcagac-atttgatttcatcac 560
||| ||| |||
Sbjct: 108954 atgctgattctatttggtgtca-accatcagatttcatcac 108915

Score = 170 bits (86), Expect = 9e-40
Identities = 194/229 (84%), Gaps = 6/229 (2%)
Strand = Plus / Minus

Query: 335 cctaccttgaggcctgagcatgctgagcaccgtcagcaccgagcgctgcctgtccgtcc 394
|||||
Sbjct: 93453 cctaccttgcaagcctgagctttctaagcgccatgagcaccgagcgctgcctgtacgtcc 93394

Query: 395 tgtggcccatctggtatcgctgccgcccgc-ccag-acacctgtcagcggtcgtgtgtgt 452
|||||
Sbjct: 93393 tgtggcccatctggttagcgctgccgccccgcacctacacctgtcagcggtcgtgtgtgt 93334

Query: 453 cctgctctgggccctgtccctactgctgagcatcttgaag-ggaagtt-ctgtggcttc 510
| |||||
Sbjct: 93333 catgctctgggccctgtctctgctgaggcgctcctgga-gtgga-gtttctgtgacttc 93276

Query: 511 ttatttagtgatggtgactctggttggtgtcagacatttgatttcatca 559
| |||||
Sbjct: 93275 ctgttagtggtgctgattctgtttggtgttaaacatcagatttcatca 93227

Score = 161 bits (81), Expect = 8e-37
Identities = 142/162 (87%), Gaps = 2/162 (1%)
Strand = Plus / Minus

Query: 587 tggttctctgtgggtccagtctggccctgctgggtcaggatcctctgtggctccaggg-gt 645
|||||
Sbjct: 70972 tggttctctgtgggtccagcctggtcctgctgatcaggattctctgtggatcccgggaaga 70913

Query: 646 ctgccactgaccaggctgtacctgaccatcctgctcacagtgtggtgttcctcctctgc 705
| |||
Sbjct: 70912 -taccgctgaccaggctgtacgtgaccatcctgctcacagtactggtcttcctcctctgt 70854

Query: 706 ggccctgccctttggcattcagtggttcctaataattatggatc 747

|||||
Sbjct: 70853 ggcctgccctttggcattcagtttttctatttttatggatc 70812

Score = 155 bits (78), Expect = 5e-35
Identities = 129/145 (88%), Gaps = 5/145 (3%)
Strand = Plus / Minus

Query: 587 tggttctctgtgggtccagtcctgtggcct-gctggtcaggatcctctgtggct-ccagggg 644
|||||
Sbjct: 47586 tggttctctgtgtgtccagcctggtcctag-tggtcaggatcctctgtggatcccagaag 47528

Query: 645 tctgccactgaccaggctgtacctgaccatcctgctcacagtgctgggtgttcctcctctg 704
|||||
Sbjct: 47527 -atgccgctgaccaggctgtacatgaccat-ctgctcacagtgctgggtcttcctcctctg 47470

Query: 705 cggcctgccctttggcattcagtg 729
|||||
Sbjct: 47469 cggcctgcccattggcattcagtg 47445

Score = 147 bits (74), Expect = 1e-32
Identities = 120/135 (88%), Gaps = 2/135 (1%)
Strand = Plus / Minus

Query: 591 tctctgtgggtccagtcctggcctgctggtcaggatcctctgtgggtccaggg-gtctgc 649
|||||
Sbjct: 93195 tctctgtgggtccagcctggtcctgctggtcaggatcctttgtgggtcccgaaga-tgc 93137

Query: 650 cactgaccaggctgtacctgaccatcctgctcacagtgctgggtgttcctcctctgcggcc 709
|||||
Sbjct: 93136 cactgaccaggctgtacgtgaccatcctgctcatagcgctgggtcttcctcctctgtggcc 93077

Query: 710 tgccctttggcattc 724
|||||
Sbjct: 93076 tgccctttggcattc 93062

Score = 145 bits (73), Expect = 5e-32
Identities = 132/151 (87%), Gaps = 4/151 (2%)
Strand = Plus / Minus

Query: 587 tggttctctgtgggtccagtcctggcctgctggtcaggatcctctgtgggtccagg-ggt 645
|||||
Sbjct: 691 tggttctctgcgggtccagcccggctcctgctggtcaggatcctttgtggatcccgaag- 633

Query: 646 ctgccac-tgaccaggctgtacctgaccatcctgctcacagtgctgggtgttcctcctctg 704
|||||
Sbjct: 632 atgcc-cttgaccaggctgtacatgaccatcctgctcacagtgctgggtcttcctcctctg 574

Query: 705 cggcctgcccttttggcattcagtggttccta 735
| |||||
Sbjct: 573 tgacctgcccttttggcattcagtgattccta 543

Score = 119 bits (60), Expect = 3e-24
Identities = 128/150 (85%), Gaps = 4/150 (2%)
Strand = Plus / Minus

Query: 106 ctgacaccttttcattgccctggctcgggctggtaggaaacg-ggtttgtgctctggctcct 164
|||||
Sbjct: 24568 ctgacacctcatcattgacctggctcgggctggcaggaaatgcag-tcatgctctggctcct 24510

Query: 165 gggcttccgcatgcgaggaacgccttctctgtctacgtcctcagcctggccggggccga 224
|||||
Sbjct: 24509 gggcttctgcatgcacagtaacaccttctctctacatcctcaacctggccagggtga 24450

Query: 225 ctctcctcttc-ctctgcttccagattataa 253
|||||
Sbjct: 24449 ctctcctctgcac-ctgcttccagattataa 24421

Score = 119 bits (60), Expect = 3e-24
Identities = 91/101 (90%), Gaps = 2/101 (1%)
Strand = Plus / Minus

Query: 138 aggaaacg-ggtttgtgctctggctcctgggcttccgcatgcgaggaacgccttctctg 196
|||||
Sbjct: 109327 aggaaacgcgg-ttgtgctctggctcctgggcttccgcatgcgaggaacgccgtctcca 109269

Query: 197 tctacgtcctcagcctggccggggccgacttctcttctc 237
|||||
Sbjct: 109268 tctacatcctcaacctggctgcggcagacttctcttctc 109228

Score = 111 bits (56), Expect = 7e-22
Identities = 102/117 (87%), Gaps = 2/117 (1%)
Strand = Plus / Minus

Query: 122 ccctggctcgggctggtaggaaacg-ggtttgtgctctggctcctgggcttccgcatgcg 180
|||||
Sbjct: 71425 cccttgctcgggctgacaggaaacgcag-ttgtgctctggctcctgggctgccgcatgcg 71367

Query: 181 aggaacgccttctctgtctacgtcctcagcctggccggggccgacttctcttctc 237
|||||
Sbjct: 71366 aggaacgccttctccatctacatcctcaacttggccgcagacttctcttctc 71310


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Query: 587      tggttctctgtgggtccagtcctggccctgctggtcaggatcctctgtgggtcc-agggggt 645
                |||||
Sbjct: 24083    tggttctctgtgggtccaccctggtcctgctgtgcaggatcatatgtggatcccagaaga 24024
```

```
Query: 646      ctgccactgaccaggctgtacctgaccatcctgctcacagtgctgggtgttcctcctctgc 705
               ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 24023    -tgccgctgaccaggctgtatgtgaccatcctgctcacagggtggtcttcctcttctgc 23965
```

Query: 706 ggcctgccctttggcattcagtggttcctaatta-tggatctg-gaaggatt 757
 ||||| | ||||| ||||| ||| | ||||| | |||||
 Sbjct: 23964 agcctgccctcagcattcagtgattcctattat-actggatc-gagaaggatt 23913

```
Query: 587      tggttctctgtgggtccagtcctggccctgctggtcaggatcctctgtggctccagg-ggt 645
               |||||
Sbjct: 108888  tggttctctgtgggtccagcctggctctgctgattaggattctctgtggatcctggaag- 108830
```

```
Query: 646      ctgccactgaccaggctgtacctgaccatcctgctcacagtgctgggtgttcctcctctgc 705
               ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 108829   atgcctctgaccgggctgtacgtgacgatcctgctcacagtgctagtcttcctactccgc 108770
```

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Query: 706      ggcctgccctttggcattcagtgg 729
                |||||
Sbjct: 108769   agcctgcccttcggcattcgggtgg 108746

```

Query: 151 gtgctctgggtccttgggcttcgcgatgcgcaggaacgccttctctgtctacgtcctcagc 210
|||||
Sbjct: 93625 gtgctctgggtccttgggcttcgcgatgcgcaggaacgccttctccatctacattttcaac 93566

```
Query: 211   ctggccggggccgacttctctt 233
            ||| || |||||
Sbjct: 93565 ctgtccatggccgacttctctt 93543
```

http://lexblast.lexgen.com/blast_results.cgi?id=18925&refresh=60

Identities = 89/102 (87%), Gaps = 4/102 (3%)
Strand = Plus / Minus

Query: 138 aggaaacg-ggtttgtgctctggctcctgggcttccgcatgcgaggaacgcct-tctct 195
||||||| || ||||||||| ||||||||| ||||||||| |||||
Sbjct: 48021 aggaaacgcgg-ttgtgctctggctcctgggcttccgcatgtgcaggaacgc-tgtctcc 47964

Query: 196 gtctacgtcctcagcctggccggggccgacttctcttctctc 237
||||| ||||||| ||||||| || ||||| ||||||||| |||||
Sbjct: 47963 atctacatcctcaacctggctcgcgccaacttctctctctc 47922

Score = 83.8 bits (42), Expect = 2e-13
Identities = 83/96 (86%), Gaps = 3/96 (3%)
Strand = Plus / Minus

Query: 154 ctctggctcctgggcttccgcatgcgaggaacgccttctctgtctacgtcctcagcctg 213
||||||| ||||||| || ||||||| ||||||| ||||| |||||
Sbjct: 1107 ctctggctcctgggattccgcctgacaggaacaccttctcctctacacctcaacctg 1048

Query: 214 gccggggccgacttctcttctctctgttccagatt 249
||||||| ||||||| || ||||||| |||||
Sbjct: 1047 gccggggccgacttc-t-t-cctctgctccagatt 1015

>AC107948.7.1.156839
Length = 156839

Score = 216 bits (109), Expect = 2e-53
Identities = 195/223 (87%), Gaps = 4/223 (1%)
Strand = Plus / Minus

Query: 320 ctgtgatgacctgtgcctaccttgaggcctgagcatgctgagcaccgtcagcaccgagc 379
||||||| || ||||||| ||||||||| ||||||||| |||||
Sbjct: 155761 ctgtgatgacctttccctactttacaggcctgagtatgctgagcgccatcagcaccgagc 155702

Query: 380 gctgcctgtccgtcctgtggcccatctggtatcgctgccgcccagacacctgtcag 439
||||||| || ||||||||| ||||||||| ||||||||| |||||||||
Sbjct: 155701 gctgcctgtctgttctgtggcccatctggtaccgctgccgcccacacacctgtcag 155642

Query: 440 cggtcgtgtgtgtcctgctctgggcccctgtccctactgctgagcat-cttgaag-ggaa 497
||||||| ||||||||| ||||||||| ||||||||| || ||||| |||||
Sbjct: 155641 cggtcgtgtgtgtcctgctctgggcccctgtccctgctgttttagtatgct-gga-gtggag 155584

Query: 498 gttctgtggcttcttatttagtgatggtgactctggttggtgt 540
||||||| ||||| ||||||||| || ||||| |||||||||
Sbjct: 155583 gttctgtgacttctgttttagtggtgctgattctagttggtgt 155541

gate
|||
gate

cgctg
|||
-gctg

ctact
| |
ctgct

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rgttg
|||||
rgttg

```

gtgg
||||
gtgg

```
gtgt
|| |
gtct
```

```

etcct
|||
etcct

```

Query: 175 atgcgcaggaacgcct-tctctgtctacgtcctcagcctggccggggccgacttctctt 233
 |||||
 Sbjct: 155894 atgcgcaggaacg-ctgtctccatctacatcctcaacctggccgcagcagacttctctt 155836

```
Query: 234      cctctgcttcagattata 252
          ||||| ||||| ||||| |||||
Sbjct: 155835 cctcagcttcagattata 155817
```

Score = 89.7 bits (45), Expect = 3e-15
Identities = 123/148 (83%), Gaps = 5/148 (3%)
Strand = Plus / Minus

```
Query: 668      tgaccatcctgctcacagtgtctgggtgttcctcctctgcggcgctgccctttggcattcagt 727
               ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 132286   tgaccatcctgctcacagtgtctgtcttcttatttgacagcctgcccttaggcattaagt 132227
```

Query: 728 ggttcctaataattatggatc-tggaaggattctgatgtcttattttggcatatt-catcc 785
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Sbjct: 132226 ggttcctattattctggatcctcgt-ggattttgatatcttcctttgtcat-ttgcaacc 132169

```
Query: 786      aagtttcagttgtcctgtcatctcttaa 813
           | ||||| ||||| ||||| |||||
Sbjct: 132168  a-gtttcagatgtcctgtcctctcttaa 132142
```

```
>AC090099.14.1.172939
      Length = 172939
```

Score = 216 bits (109), Expect = 2e-53
Identities = 195/223 (87%), Gaps = 4/223 (1%)
Strand = Plus / Minus

Query: 320 ctgtgatgacctgtgcctaccttgcaggcctgagcatgctgagcaccgtcagcacccgagc 379
|||||
Sbjct: 77620 ctgtgatgacctttccctactttacaggcctgagtatgctgagcgccatcagcacccgagc 77561

```
Query: 380      gctgcctgtccgctcctgtggcccatctggtatcgctgccgcccccagacacctgtcag 439
                ||||||||| | ||||||||||||||| ||||||||||||||| |||||||||
Sbjct: 77560    gctgcctgtctgttctgtggcccatctggtaccgctgccgccccccacacacctgtcag 77501
```

Query: 440 cggtcgtgctgtgcctcgtctgggccctgtccctactgctgagcat-cttggaag-ggaa 497
|||||
Sbjct: 77500 cggtcgtgctgtgcctcgtctgggccctgtccctgctgttagtatgct-gga-gtggag 77443

```
Query: 498      gttctgtggcttcttatttagtgatggtgactctggttggtgt 540
               ||||| | | | | | | | | | | | | | | | |
Sbjct: 77442    gttctgtgacttcctgttttagtggtgctgattctagttggtgt 77400
```

On

Qu.

0

•

Only

Quesada

0

Score = 172 bits (87), Expect = 2e-40
Identities = 130/144 (90%), Gaps = 2/144 (1%)
Strand = Plus / Minus

Query: 587 tgggttctctgtgggtccagtcctggccctgctgggtcaggatcctctgtgggtccaggg-gt 645
 |||||
Sbjct: 113407 tgggttctctgtgggtccagcctggctcctgctgggtcaggattctctgtggatcccggaaga 113348

Query: 646 ctgccactgaccaggctgtacctgaccatcctgctcacagtgctgggtgttcctcctctgc 705
 |||||
Sbjct: 113347 -tgccgctgaccaggctgtacgtgaccatcctcctcacagtgctgggtcttcctcctctgt 113289

Query: 706 ggccctgccctttggcattcagtg 729
 |||||
Sbjct: 113288 ggccctgccctttggcattcagtg 113265

Score = 163 bits (82), Expect = 2e-37
Identities = 125/139 (89%), Gaps = 2/139 (1%)
Strand = Plus / Minus

Query: 587 tgggttctctgtgggtccagtcctggccctgctgggtcaggatcctctgtgggtccagg-ggt 645
 |||||
Sbjct: 77353 tgggttctctgtgtttccagcctggctcctgctgggtcaggatcctctgtggatcccggaag- 77295

Query: 646 ctgccactgaccaggctgtacctgaccatcctgctcacagtgctgggtgttcctcctctgc 705
 |||||
Sbjct: 77294 atgccgctgaccaggctgtacgtgaccatcctgctcacagtgctgggtcttcctcctctgc 77235

Query: 706 ggccctgccctttggcattc 724
 |||||
Sbjct: 77234 ggccctgcccttcggcattc 77216

Score = 159 bits (80), Expect = 3e-36
Identities = 172/202 (85%), Gaps = 4/202 (1%)
Strand = Plus / Minus

Query: 280 ttctgttccatctccatc-aatttccctagcttcttcaccactgtgatga-cctgtgcct 337
 |||||
Sbjct: 97620 ttctcttccatctccatctacttt-cctagcttcttcaatgctgtgatgatcct-ttcct 97563

Query: 338 accttgaggcctgagcatgctgagcaccgtcagcaccgagcgctgcctgtccgtcctgt 397
 |||||
Sbjct: 97562 accttgaggggctgagcatgctaagcaccatcagcatcaaactgcataatctgcctgt 97503

Query: 398 ggcccatctgggtatcgctgccgcgcgccagacacctgtcagcggtcgtgtgtgcctgc 457
 |||||
Sbjct: 97502 ggcccatctgggtaccactgccgtcgccccacacacctgtcagcagtcctgtgtgccctgc 97443

Query: 458 tctgggcccctgtccctactgct 479
|||||
Sbjct: 97442 tctgggccccgtccctgctgct 97421

Score = 139 bits (70), Expect = 3e-30
Identities = 191/230 (83%), Gaps = 8/230 (3%)
Strand = Plus / Minus

Query: 587 tggttctctgtgggtccagtctggccctgctgggtcaggatcctctgtggctcc-agggggt 645
|||||
Sbjct: 97313 tggttctctgtgggtccaacctggttctgctagtcaggatcctctgtgggtcccagcaga 97254

Query: 646 ctgccactgaccaggctgtacctgaccatcctgctcacagtgctgggtgttcctcctctgc 705
|||||
Sbjct: 97253 -tgccactgagcgggctgtagatgaccatcttgctcacagtgctgggtgtttctcctatgc 97195

Query: 706 ggccctgccctttggcattcagtggttcctaataattatggatctggaagga-ttctgatgt 764
|||||
Sbjct: 97194 agcctgccccttggcattcagtgattcctgttattctgga-ctgaaaaaactt-tcatgt 97137

Query: 765 cttatatttggcatattcatccaagtttcagttgtcctg-tcatctcttaa 813
|||
Sbjct: 97136 cttcctttgtcatgttcttcca-gtttcagttgtc-tggtcctctcttaa 97089

Score = 129 bits (65), Expect = 3e-27
Identities = 121/139 (87%), Gaps = 4/139 (2%)
Strand = Plus / Minus

Query: 116 tcattgccctggtcgggctggtaggaaacg-ggtttgtgctctggctcctgggcttccgc 174
|||||
Sbjct: 77812 tcatttcccttgtcggactgacaggaaacgcgg-ttgtgctctggctcctgggctaccgc 77754

Query: 175 atgcgaggaacgcct-tctctgtctacgtcctcagcctggccggggccgacttctctt 233
|||||
Sbjct: 77753 atgcgaggaacg-ctgtctccatctacatcctcaacctggccgcagcagacttctctt 77695

Query: 234 cctctgcttccagattata 252
|||
Sbjct: 77694 cctcagcttccagattata 77676

Score = 109 bits (55), Expect = 3e-21
Identities = 90/101 (89%), Gaps = 4/101 (3%)
Strand = Plus / Minus

```
Query: 196      gtctacgtcctcagcctggccggggccgacttctcttct 236
               ||||| ||||| ||||| || ||||| ||||| ||||| |||||
Sbjct: 113786  atctacatcctcaacctggctcgcgcccgacttctcttct 113746
```

Score = 89.7 bits (45), Expect = 3e-15
Identities = 123/148 (83%), Gaps = 5/148 (3%)
Strand = Plus / Minus

Query: 728 ggttcctaataattatggatc-tggaaggattctgatgtcttattttggcatatt-catcc 785
 |||||
 Sbjct: 54089 ggttcctattattctggatcctcgt-ggattttgatatacttcctttgtcat-ttgaacc 54032

```
Query: 786      aagtttcagttgtcctgtcatctcttaa 813
              | ||||| ||||| ||||| |||||
Sbjct: 54031    a-gtttcagatgtcctgtcctctcttaa 54005
```

Score = 81.8 bits (41), Expect = 6e-13
Identities = 50/53 (94%)
Strand = Plus / Minus

Query: 587 tggttctctgtggtccagtcctggcctgctgggcaggatcctctgtggctcc 639
 |||||
Sbjct: 54228 tggttctctgtgagtccagcctggctcctgctgggcaggatcctctgtggctcc 54176

```
>AC103974.6.1.189230
      Length = 189230
```

Score = 212 bits (107), Expect = 3e-52
Identities = 214/249 (85%), Gaps = 4/249 (1%)
Strand = Plus / Plus

Query: 313 ttcaccactgtgatgacctgtgc-ctaccttgaggcctgagcatgctgagcaccgtcag 371
 |||
 Sbjct: 17860 ttcaccactgtgatgacct-ttctctactttacaggcctgagcatgctgggctccatcag 17918

```
Query: 372   caccgagcgtgcctgtccgtcctgtggcccatctggtatcgctgccgccgccccagaca 431
           ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 17919 caccaagcactgcctgtccatcctgtggcccatctagtagcgctgccaccacccccacaca 17978
```


Query: 432 cctgtcagcggctcgtgtgtgtcctgctctgggcctgtccctactgctgagcatcttgga 491
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 17979 cctgtcagcagtcgtgtgt--cctgctctgggcctgtccctgctgcagagcatcctgga 18036

Query: 492 aggggaagttctgtggccttcttatttagtgatgggtgactctgggttggtgtcagacatttga 551
| ||| ||||| ||||| ||| ||||| || ||||| || ||||| ||||| ||||| |||||
Sbjct: 18037 atggatgttctgtggccttctgtctagtgggtgctgattctgtttggtgtgaaacatcaga 18096

Query: 552 tttcatcac 560
|||||||
Sbjct: 18097 tttcatcac 18105

Score = 145 bits (73), Expect = 5e-32
Identities = 132/151 (87%), Gaps = 4/151 (2%)
Strand = Plus / Plus

Query: 587 tggttctctgtgggtccagtcctggccctgctgggtcaggatcctctgtgggtccagg-ggt 645
||||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 18132 tggttctctgcgggtccagccccggtcctgctgggtcaggatccttctgtggatcccgaag- 18190

Query: 646 ctgccac-tgaccaggctgtacctgaccatcctgctcacagtgctgggtgttcctcctctg 704
|||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 18191 atgcc-cttgaccaggctgtacatgaccatcctgctcagagtgctgggtcttcctcctctg 18249

Query: 705 cggcctgccctttggcattcagtggttccta 735
| ||||| ||||| ||||| ||||| |||||
Sbjct: 18250 tgacctgccctttggcattcagtgattccta 18280

Score = 91.7 bits (46), Expect = 6e-16
Identities = 84/96 (87%), Gaps = 3/96 (3%)
Strand = Plus / Plus

Query: 154 ctctggctcctgggcttccgcatgcgcaggaacgccttctctgtctacgtcctcagcctg 213
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 17716 ctctggctcctgggattccgcatgcacaggaacaccttctccctctacaccctcaacctg 17775

Query: 214 gccggggccgacttcctcttctctgttccagatt 249
||||||| ||||| || ||||| ||||| ||||| |||||
Sbjct: 17776 gccggggccgacttc-t-t-cctctgtcccagatt 17808

Database: Homo_sapiens.latestgp.masked.fa
Posted date: Apr 17, 2003 4:52 PM
Number of letters in database: 200,810,911,373
Number of sequences in database: 33,840

Lambda K H

1.37 0.711 1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 0, Extension: 0

Number of Hits to DB: 0

length of query: 1628

length of database: 200,810,911,373

effective HSP length: 21

effective length of query: 792

effective search space used: 0

T: 0

A: 0

X1: 0 (0.0 bits)

X2: 20 (39.6 bits)

S1: 12 (24.3 bits)

S2: 38 (75.8 bits)

EXHIBIT "C"

>NM_054030 ACCESSION:NM_054030 NID: gi 16876450 ref NM_054030.1 Homo sapiens
G protein-coupled receptor MRGX2 (MRGX2), mRNA
Length = 993

Score = 1536 bits (775), Expect = 0.0
Identities = 804/813 (98%), Gaps = 1/813 (0%)
Strand = Plus / Plus

```
Query: 1   atggatccaaccaccccggcctggggaacagaaagtacaacagtgaatggaaatgaccaa 60
          |||
Sbjct: 1   atggatccaaccaccccggcctggggaacagaaagtacaacagtgaatggaaatgaccaa 60

Query: 61   gcccttcttctgctttgtggcaaggagaccctgatcccggtcttctctgatccttttcatt 120
          |||
Sbjct: 61   gcccttcttctgctttgtggcaaggagaccctgatcccggtcttctctgatccttttcatt 120

Query: 121  gccctggtcgggctggttaggaaacgggtttgtgctctggctcctgggcttccgcatgcgc 180
          |||
Sbjct: 121  gccctggtcgggctggttaggaaacgggtttgtgctctggctcctgggcttccgcatgcgc 180

Query: 181  aggaacgccttctctgtctacgtcctcagcctggccggggccgacttctcttctctctgc 240
          |||
Sbjct: 181  aggaacgccttctctgtctacgtcctcagcctggccggggccgacttctcttctctctgc 240

Query: 241  ttccagattataaattgcctggtgtacctcagtaacttcttctgttccatctccatcaat 300
          |||
Sbjct: 241  ttccagattataaattgcctggtgtacctcagtaacttcttctgttccatctccatcaat 300

Query: 301  ttccctagcttcttcaccactgtgatgacctgtgcctaccttgcaggcctgagcatgctg 360
          |||
Sbjct: 301  ttccctagcttcttcaccactgtgatgacctgtgcctaccttgcaggcctgagcatgctg 360

Query: 361  agcaccgtcagcaccgagcgctgcctgtccgtcctgtggcccatctggtatcgctgccgc 420
          |||
Sbjct: 361  agcaccgtcagcaccgagcgctgcctgtccgtcctgtggcccatctggtatcgctgccgc 420

Query: 421  cgccccagacacctgtcagcggtcggtgtgtgctctgctctgggccctgtccctactgctg 480
          |||
Sbjct: 421  cgccccagacacctgtcagcggtcggtgtgtgctctgctctgggccctgtccctactgctg 480

Query: 481  agcatcttgaagggaagtctgtggcttcttatttagtgatggtgactctggttggtgt 540
          |||
Sbjct: 481  agcatcttgaagggaagtctgtggcttcttatttagtgatggtgactctggttggtgt 540

Query: 541  cagacatttgatttcatcactgcagcggtggctgannnnnnnattcatggttctctgtggg 600
          |||
Sbjct: 541  cagacatttgatttcatcactgcagcggtggctgatttttttattcatggttctctgtggg 600

Query: 601  tccagtctggccctgctggtcaggatcctctgtggctccaggggtctgccactgaccagg 660
```


>hGPR_32_ORF_03

Length = 813

Score = 1570 bits (792), Expect = 0.0

Identities = 806/813 (99%)

Strand = Plus / Plus

```
Query: 1  atggatccaaccaccccggcctggggaacagaaagtacaacagtgaatggaaatgaccaa 60
          |||
Sbjct: 1  atggatccaaccaccccggcctggggaacagaaagtacaacagtgaatggaaatgaccaa 60

Query: 61  gcccttcttctgctttgtggcaaggagaccctgatcccggtcttctctgatccttttcatt 120
          |||
Sbjct: 61  gcccttcttctgctttgtggcaaggagaccctgatcccggtcttctctgatccttttcatt 120

Query: 121 gccctggtcgggctggtaggaaacgggtttgtgctctggctcctgggcttcgcgatgcgc 180
          |||
Sbjct: 121 gccctggtcgggctggtaggaaacgggtttgtgctctggctcctgggcttcgcgatgcgc 180

Query: 181 aggaacgccttctctgtctacgtcctcagcctggccggggccgacttctcttctctctgc 240
          |||
Sbjct: 181 aggaacgccttctctgtctacgtcctcagcctggccggggccgacttctcttctctctgc 240

Query: 241 ttccagattataaattgcctgggtgtacctcagtaacttcttctgttccatctccatcaat 300
          |||
Sbjct: 241 ttccagattataaattgcctgggtgtacctcagtaacttcttctgttccatctccatcaat 300

Query: 301 ttccctagcttcttcaccactgtgatgacctgtgcctaccttgaggcctgagcatgctg 360
          |||
Sbjct: 301 ttccctagcttcttcaccactgtgatgacctgtgcctaccttgaggcctgagcatgctg 360

Query: 361 agcaccgtcagcaccgagcgctgcctgtccgtcctgtggcccatctggatcgctgccgc 420
          |||
Sbjct: 361 agcaccgtcagcaccgagcgctgcctgtccgtcctgtggcccatctggatcgctgccgc 420

Query: 421 cgccccagacacctgtcagcggtcgtgtgtgtcctgctctgggccctgtccctactgctg 480
          |||
Sbjct: 421 cgccccagacacctgtcagcggtcgtgtgtgtcctgctctgggccctgtccctactgctg 480

Query: 481 agcatcttggaagggaagtctctgtggcttcttatttagtgatgggtgactctggttggtgt 540
          |||
Sbjct: 481 agcatcttggaagggaagtctctgtggcttcttatttagtgatgggtgactctggttggtgt 540

Query: 541 cagacatttgatttcatcactgcagcggtggctgannnnnnnattcatggttctctgtggg 600
          |||
Sbjct: 541 cagacatttgatttcatcactgcagcggtggctgatttttttattcatggttctctgtggg 600

Query: 601 tccagtctggccctgctgggtcaggatcctctgtggctccaggggtctgccactgaccagg 660
          |||
```

Sbjct: 601 tccagtctggccctgctgggtcaggatcctctgtgggtccaggggtctgccactgaccagg 660

Query: 661 ctgtacctgaccatcctgctcacagtgctgggtgttcctcctctgcggcctgccctttggc 720
|||||

Sbjct: 661 ctgtacctgaccatcctgctcacagtgctgggtgttcctcctctgcggcctgccctttggc 720

Query: 721 attcagtgggttcctaataattatggatctggaaggattctgatgtcttattttggcatatt 780
|||||

Sbjct: 721 attcagtgggttcctaataattatggatctggaaggattctgatgtcttattttggcatatt 780

Query: 781 catccaagtttcagttgtcctgtcatctcttaa 813
|||||

Sbjct: 781 catccaagtttcagttgtcctgtcatctcttaa 813

NCBI Nucleotide

PubMed Nucleotide Protein Genome Structure PopSet Taxonomy OMIM Bio

Search for

Limits Preview/Index History Clipboard Details

Display

☐ 1: NM_054030. Homo sapiens G pr...
[gi:16876450]

MapView, Related Sequences, Protein, PubMed, Taxonomy,
LinkOut

LOCUS MRGX2 993 bp mRNA linear PRI 09-FEB-2002
DEFINITION Homo sapiens G protein-coupled receptor MRGX2 (MRGX2), mRNA.
ACCESSION NM_054030
VERSION NM_054030.1 GI:16876450
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 993)
AUTHORS Dong,X., Han,S., Zylka,M.J., Simon,M.I. and Anderson,D.J.
TITLE A diverse family of GPCRs expressed in specific subsets of
nociceptive sensory neurons
JOURNAL Cell 106 (5), 619-632 (2001)
MEDLINE 21435808
PUBMED 11551509
COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
NCBI review. The reference sequence was derived from AY042214.1.
FEATURES
source
1..993
/organism="Homo sapiens"
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/chromosome="11"
/map="11p15.1"
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SILEGKFCGFLFSDGDSGWCQTFDFITAAWLIFLFMVLCGSSALLVRILCGSRGLPL
TRLYLTIILLTVLVFLLCGLPFGIQWFLILWIWKDSVDLFCIHHPVSVVLSLSSANP
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misc_feature
139..429
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/note="7tm_1; Region: 7 transmembrane receptor (rhodopsin
family)"
/db_xref="CDD:pfam00001"

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BASE COUNT      165 a      283 c      257 g      288 t
ORIGIN
   1 atggatccaa ccaccccggc ctggggaaca gaaagtacaa cagtgaatgg aaatgaccaa
  61 gcccttcttc tgctttgtgg caaggagacc ctgatcccgg tcttcctgat ccttttcatt
 121 gccctggtcg ggctggtagg aaacggggtt gtgctctggc tcctgggctt ccgcatgcgc
 181 aggaacgcct tctctgtcta cgtcctcagc ctggccgggg cgcacttcct cttcctctgc
 241 ttccagatta taaattgcct ggtgtacctc agtaacttct tctgttccat ctccatcaat
 301 ttccctagct tcttcaccac tgtgatgacc tgtgcctacc ttgcaggcct gagcatgctg
 361 agcaccgtca gcaccgagcg ctgcctgtcc gtcctgtggc ccatctggta tcgctgccgc
 421 cgccccagac acctgtcagc ggtcgtgtgt gtcctgctct gggccctgtc cctactgctg
 481 agcatcttgg aaggggaagt ctgtggcttc ttatttagtg atggtgactc tggttggtgt
 541 cagacatttg atttcatcac tgcagcgtgg ctgatttttt tattcatggg tctctgtggg
 601 tccagtctgg ccttctgtgg caggatcctc tgtggctcca ggggtctgcc actgaccagg
 661 ctgtacctga ccatactgct cacagtgtct gtgttctctc tctgcggcct gccctttggc
 721 attcagtggt tcctaataatt atggatctgg aaggattctg atgtcttatt ttgtcatatt
 781 catccagttt cagttgtcct gtcatactct aacagcagtg ccaaccccat catttaactc
 841 ttcgtgggct cttttaggaa gcagtggcgg ctgcagcagc cgatcctcaa gctggctctc
 901 cagagggctc tgcaggacat tgctgagggt gatcacagtg aaggatgctt ccgtcagggc
 961 accccggaga tgtcgagaag cagtctggtg tag
```

//

Revised: July 5, 2002.

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Jul 16 2002 16:59:14

>hGPR_32_ORF_03

Length = 813

Score = 1570 bits (792), Expect = 0.0

Identities = 806/813 (99%)

Strand = Plus / Plus

```
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          |||
Sbjct: 1   atggatccaaccacccccggcctggggaacagaaagtacaacagtgaatggaaatgaccaa 60

Query: 61   gcccttcttctgctttgtggcaaggagaccctgatcccggctcttctgatccttttcatt 120
          |||
Sbjct: 61   gcccttcttctgctttgtggcaaggagaccctgatcccggctcttctgatccttttcatt 120

Query: 121  gccctggtcgggctggtaggaaacgggtttgtgctctggctcctgggcttccgcatgcgc 180
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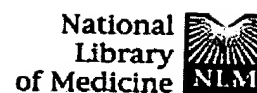
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PRESS**A diverse family of GPCRs expressed in specific subsets of nociceptive sensory neurons.****Dong X, Han S, Zylka MJ, Simon MI, Anderson DJ.**

Division of Biology 216-76, California Institute of Technology, Pasadena, CA 91125, USA.

In vertebrates, peripheral chemosensory neurons express large families of G protein-coupled receptors (GPCRs), reflecting the diversity and specificity of stimuli they detect. However, somatosensory neurons, which respond to chemical, thermal, or mechanical stimuli, are more broadly tuned. Here we describe a family of approximately 50 GPCRs related to Mas1, called mrgs, a subset of which is expressed in specific subpopulations of sensory neurons that detect painful stimuli. The expression patterns of mrgs thus reveal an unexpected degree of molecular diversity among nociceptive neurons. Some of these receptors can be specifically activated in heterologous cells by RFamide neuropeptides such as NPFF and NPAF, which are analgesic in vivo. Thus, mrgs may regulate nociceptor function and/or development, including the sensation or modulation of pain.

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